

ABSTRACT

The invention overcomes deficiencies in the prior art by identifying a locus associated with average weaning weight and carcass weight of cattle. The locus was found during studies carried out by the inventors using a polymorphic TG-repeat microsatellite located 90 base pairs upstream from a major transcription start site in the bovine growth hormone receptor gene. Use of this marker and other genetic markers in linkage disequilibrium with the locus allows implementation of selection and breeding schemes for improvement of cattle performance. Marker-assisted selection with the genetic markers will allow avoidance of potentially costly phenotypic testing associated with traditional breeding schemes.